

RAW SEQUENCE LISTING

DATE: 07/16/2001

PATENT APPLICATION: US/09/724,126A

TIME: 14:15:51

Input Set : A:\35966Aseq.txt

Output Set: N:\CRF3\07162001\I724126A.raw

5 <110> APPLICANT: Han, Hui-Quan
6 Kwak, Keith
9 <120> TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family
11 <130> FILE REFERENCE: 01017/35966A
13 <140> CURRENT APPLICATION NUMBER: US 09/724,126A
14 <141> CURRENT FILING DATE: 2000-11-28
16 <150> PRIOR APPLICATION NUMBER: US 60/187,211
17 <151> PRIOR FILING DATE: 1999-03-01
19 <160> NUMBER OF SEQ ID NOS: 29
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 6308
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (696)..(5942)
32 <400> SEQUENCE: 1

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37	ccaaaggctt atcatctgtc ttccacttat ccaacaagct gctatggcca ctgcctgtgc	180
39	cgcacctgga accaccgcca gcccactac tgccctccact accactgggt ctcccaccct	240
41	gatcagctgc ttgctgctgc catcttatcc gcttctgcct gttctgagta aatgtataca	300
43	caccttgga accaccattc tactttctgt gtctatgaat ttgactactc tagctggatc	360
45	ccgagctttt ttgtacacat gtgcaagtgc ccacggggta gaatcctaaa aatagaagat	420
47	gtatgcaaca gttcccagca ccaaaccag atatacaacc attcagctac caagagctac	480
49	gcctgataaa ttagagggga aaaaaaaaaat ctccagtcctc ttacagtcgt gacgcttgct	540
51	tccgggaagc gggccggaag ccactcctcg agtctgcgtc aaaccgcact tcaggggccc	600
53	tcgtaaaagt gtcgtccctg tctctccgac cggccacagg tttccgcttg cctctggccc	660
55	ggggtcggca actgcaggcg tcagtttccc tcaag atg gcg gac gag gag gct	713
56	Met Ala Asp Glu Glu Ala	
57	1 5	
59	gga ggt act gag agg atg gaa atc agc gcg gag tta ccc cag acc cct	761
60	Gly Gly Thr Glu Arg Met Glu Ile Ser Ala Glu Leu Pro Gln Thr Pro	
61	10 15 20	
63	cag cgt ctg gca tct tgg tgg gat cag caa gtt gat ttt tat act gct	809
64	Gln Arg Leu Ala Ser Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala	
65	25 30 35	
67	ttc ttg cat cat ttg gca caa ttg gtg cca gaa att tac ttt gct gaa	857
68	Phe Leu His His Leu Ala Gln Leu Val Pro Glu Ile Tyr Phe Ala Glu	
69	40 45 50	
71	atg gac cca gac ttg gaa aag cag gag gaa agt gta caa atg tca ata	905
72	Met Asp Pro Asp Leu Glu Lys Gln Glu Glu Ser Val Gln Met Ser Ile	
73	55 60 65 70	
75	ttc act cca ctg gaa tgg tac tta ttt gga gaa gat cca gat att tgc	953
76	Phe Thr Pro Leu Glu Trp Tyr Leu Phe Gly Glu Asp Pro Asp Ile Cys	
77	75 80 85	

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79	tta	gag	aaa	ttg	aag	cac	agt	gga	gca	ttt	cag	ctt	tgt	ggg	agg	gtt	1001
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81				90					95					100			
83	ttc	aaa	agt	gga	gag	aca	acc	tat	tct	tgc	agg	gat	tgt	gca	att	gat	1049
84	Phe	Lys	Ser	Gly	Glu	Thr	Thr	Tyr	Ser	Cys	Arg	Asp	Cys	Ala	Ile	Asp	
85			105					110					115				
87	cca	aca	tgt	gta	ctc	tgt	atg	gac	tgc	ttc	cag	gac	agt	gtt	cat	aaa	1097
88	Pro	Thr	Cys	Val	Leu	Cys	Met	Asp	Cys	Phe	Gln	Asp	Ser	Val	His	Lys	
89			120				125					130					
91	aat	cat	cgt	tac	aag	atg	cat	act	tct	act	gga	gga	ggg	ttc	tgt	gac	1145
92	Asn	His	Arg	Tyr	Lys	Met	His	Thr	Ser	Thr	Gly	Gly	Gly	Phe	Cys	Asp	
93	135					140					145				150		
95	tgt	gga	gac	aca	gag	gca	tgg	aaa	act	ggc	cct	ttt	tgt	gta	aat	cat	1193
96	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Thr	Gly	Pro	Phe	Cys	Val	Asn	His	
97				155					160				165				
99	gaa	cct	gga	aga	gca	ggt	act	ata	aaa	gag	aat	tca	cgc	tgt	ccg	ttg	1241
100	Glu	Pro	Gly	Arg	Ala	Gly	Thr	Ile	Lys	Glu	Asn	Ser	Arg	Cys	Pro	Leu	
101				170					175				180				
103	aat	gaa	gag	gta	att	gtc	caa	gcc	agg	aaa	ata	ttt	cct	tca	gtg	ata	1289
104	Asn	Glu	Glu	Val	Ile	Val	Gln	Ala	Arg	Lys	Ile	Phe	Pro	Ser	Val	Ile	
105			185				190					195					
107	aaa	tat	gtc	gta	gaa	atg	act	ata	tgg	gaa	gag	gaa	aaa	gaa	ctg	cct	1337
108	Lys	Tyr	Val	Val	Glu	Met	Thr	Ile	Trp	Glu	Glu	Glu	Lys	Glu	Leu	Pro	
109			200				205					210					
111	cct	gaa	ctc	cag	ata	agg	gag	aaa	aat	gaa	aga	tac	tat	tgt	gtc	ctt	1385
112	Pro	Glu	Leu	Gln	Ile	Arg	Glu	Lys	Asn	Glu	Arg	Tyr	Tyr	Cys	Val	Leu	
113	215					220					225				230		
117	ttc	aat	gat	gaa	cac	cat	tca	tat	gac	cac	gtc	ata	tac	agc	cta	caa	1433
118	Phe	Asn	Asp	Glu	His	His	Ser	Tyr	Asp	His	Val	Ile	Tyr	Ser	Leu	Gln	
119				235					240				245				
121	aga	gct	ctt	gac	tgt	gag	ctc	gca	gag	gcc	cag	ttg	cat	acc	act	gcc	1481
122	Arg	Ala	Leu	Asp	Cys	Glu	Leu	Ala	Glu	Ala	Gln	Leu	His	Thr	Thr	Ala	
123				250					255				260				
126	att	gac	aaa	gag	ggt	cgt	cgg	gct	gtt	aaa	gcg	gga	gct	tat	gct	gct	1529
127	Ile	Asp	Lys	Glu	Gly	Arg	Arg	Ala	Val	Lys	Ala	Gly	Ala	Tyr	Ala	Ala	
128			265				270					275					
130	tgc	cag	gaa	gca	aag	gaa	gat	ata	aag	agt	cat	tca	gaa	aat	gtc	tct	1577
131	Cys	Gln	Glu	Ala	Lys	Glu	Asp	Ile	Lys	Ser	His	Ser	Glu	Asn	Val	Ser	
132			280				285					290					
134	caa	cat	cca	ctt	cat	gta	gaa	gta	tta	cac	tca	gag	att	atg	gct	cat	1625
135	Gln	His	Pro	Leu	His	Val	Glu	Val	Leu	His	Ser	Glu	Ile	Met	Ala	His	
136	295					300					305				310		
138	cag	aaa	ttt	gct	ttg	cgt	ctt	ggt	tcc	tgg	atg	aac	aaa	att	atg	agc	1673
139	Gln	Lys	Phe	Ala	Leu	Arg	Leu	Gly	Ser	Trp	Met	Asn	Lys	Ile	Met	Ser	
140				315					320				325				
142	tat	tca	agt	gac	ttt	agg	cag	atc	ttt	tgc	caa	gca	tgc	ctt	aga	gaa	1721
143	Tyr	Ser	Ser	Asp	Phe	Arg	Gln	Ile	Phe	Cys	Gln	Ala	Cys	Leu	Arg	Glu	
144				330					335				340				
146	gaa	cct	gac	tcg	gag	aat	ccc	tgt	ctc	ata	agc	agg	tta	atg	ctt	tgg	1769

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147	Glu	Pro	Asp	Ser	Glu	Asn	Pro	Cys	Leu	Ile	Ser	Arg	Leu	Met	Leu	Trp	
148			345					350					355				
150	gat	gca	aag	ctt	tat	aaa	ggt	gcc	cgt	aag	atc	ctt	cat	gaa	ttg	atc	1817
151	Asp	Ala	Lys	Leu	Tyr	Lys	Gly	Ala	Arg	Lys	Ile	Leu	His	Glu	Leu	Ile	
152		360					365					370					
154	ttc	agc	agt	ttt	ttt	atg	gag	atg	gaa	tac	aaa	aaa	ctc	ttt	gct	atg	1865
155	Phe	Ser	Ser	Phe	Phe	Met	Glu	Met	Glu	Tyr	Lys	Lys	Leu	Phe	Ala	Met	
156	375					380					385					390	
158	gaa	ttt	gtg	aag	tat	tat	aaa	caa	ctg	cag	aaa	gaa	tat	atc	agt	gat	1913
159	Glu	Phe	Val	Lys	Tyr	Tyr	Lys	Gln	Leu	Gln	Lys	Glu	Tyr	Ile	Ser	Asp	
160				395						400					405		
162	gat	cat	gac	aga	agt	atc	tct	ata	act	gca	ctt	tca	ggt	cag	atg	ttt	1961
163	Asp	His	Asp	Arg	Ser	Ile	Ser	Ile	Thr	Ala	Leu	Ser	Val	Gln	Met	Phe	
164			410						415					420			
166	act	ggt	cct	act	ctg	gct	cga	cat	ctt	att	gaa	gag	cag	aat	ggt	atc	2009
167	Thr	Val	Pro	Thr	Leu	Ala	Arg	His	Leu	Ile	Glu	Glu	Gln	Asn	Val	Ile	
168		425					430						435				
170	tct	gtc	att	act	gaa	act	ctg	cta	gaa	ggt	tta	cct	gag	tac	ttg	gac	2057
171	Ser	Val	Ile	Thr	Glu	Thr	Leu	Leu	Glu	Val	Leu	Pro	Glu	Tyr	Leu	Asp	
172		440					445					450					
175	agg	aac	aat	aaa	ttc	aac	ttc	cag	ggt	tat	agc	cag	gac	aaa	ttg	gga	2105
176	Arg	Asn	Asn	Lys	Phe	Asn	Phe	Gln	Gly	Tyr	Ser	Gln	Asp	Lys	Leu	Gly	
177	455				460					465						470	
179	aga	gta	tat	gca	gta	ata	tgt	gac	cta	aag	tat	atc	ctg	atc	agc	aaa	2153
180	Arg	Val	Tyr	Ala	Val	Ile	Cys	Asp	Leu	Lys	Tyr	Ile	Leu	Ile	Ser	Lys	
181				475					480					485			
183	ccc	aca	ata	tgg	aca	gaa	aga	tta	aga	atg	cag	ttc	ctt	gaa	ggt	ttt	2201
184	Pro	Thr	Ile	Trp	Thr	Glu	Arg	Leu	Arg	Met	Gln	Phe	Leu	Glu	Gly	Phe	
185			490						495					500			
188	cga	tct	ttt	ttg	aag	att	ctt	acc	tgt	atg	cag	gga	atg	gaa	gaa	atc	2249
189	Arg	Ser	Phe	Leu	Lys	Ile	Leu	Thr	Cys	Met	Gln	Gly	Met	Glu	Glu	Ile	
190			505					510					515				
192	cga	aga	cag	ggt	ggg	caa	cac	att	gaa	gtg	gat	cct	gat	tgg	gag	gct	2297
193	Arg	Arg	Gln	Val	Gly	Gln	His	Ile	Glu	Val	Asp	Pro	Asp	Trp	Glu	Ala	
194		520				525						530					
196	gcc	att	gct	ata	cag	atg	caa	ttg	aag	aat	att	tta	ctc	atg	ttc	caa	2345
197	Ala	Ile	Ala	Ile	Gln	Met	Gln	Leu	Lys	Asn	Ile	Leu	Leu	Met	Phe	Gln	
198	535				540					545					550		
200	gag	tgg	tgt	gct	tgt	gat	gaa	gaa	ctc	tta	ctt	gtg	gct	tat	aaa	gaa	2393
201	Glu	Trp	Cys	Ala	Cys	Asp	Glu	Glu	Leu	Leu	Val	Ala	Tyr	Lys	Glu		
202				555					560					565			
204	tgt	cac	aaa	gct	gtg	atg	agg	tgc	agt	acc	agt	ttc	ata	tct	agt	agc	2441
205	Cys	His	Lys	Ala	Val	Met	Arg	Cys	Ser	Thr	Ser	Phe	Ile	Ser	Ser	Ser	
206			570					575					580				
208	aag	aca	gta	gta	caa	tcg	tgt	gga	cat	agt	ttg	gaa	aca	aag	tcc	tac	2489
209	Lys	Thr	Val	Val	Gln	Ser	Cys	Gly	His	Ser	Leu	Glu	Thr	Lys	Ser	Tyr	
210		585					590					595					
212	aga	gta	tct	gag	gat	ctt	gta	agc	ata	cat	ctg	cca	ctc	tct	agg	acc	2537
213	Arg	Val	Ser	Glu	Asp	Leu	Val	Ser	Ile	His	Leu	Pro	Leu	Ser	Arg	Thr	

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218	615 620 625 630			
220	ctg cat gaa ttt gtg tct ttt gag gac ttt caa gta gag gta cta gtg	2633		
221	Leu His Glu Phe Val Ser Phe Glu Asp Phe Gln Val Glu Val Leu Val			
222	635 640 645			
224	gaa tat cct tta cgt tgt ctg gtg ttg gtt gcc cag gtt gtt gct gag	2681		
225	Glu Tyr Pro Leu Arg Cys Leu Val Leu Val Ala Gln Val Val Ala Glu			
226	650 655 660			
228	atg tgg cga aga aat gga ctg tct ctt att agc cag gtg ttt tat tac	2729		
229	Met Trp Arg Arg Asn Gly Leu Ser Leu Ile Ser Gln Val Phe Tyr Tyr			
230	665 670 675			
233	caa gat gtt aag tgc aga gaa gaa atg tat gat aaa gat atc atc atg	2777		
234	Gln Asp Val Lys Cys Arg Glu Glu Met Tyr Asp Lys Asp Ile Ile Met			
235	680 685 690			
237	ctt cag att ggt gca tct tta atg gat ccc aat aag ttc ttg tta ctg	2825		
238	Leu Gln Ile Gly Ala Ser Leu Met Asp Pro Asn Lys Phe Leu Leu Leu			
239	695 700 705 710			
241	gta ctt cag agg tat gaa ctt gcc gag gct ttt aac aag acc ata tct	2873		
242	Val Leu Gln Arg Tyr Glu Leu Ala Glu Ala Phe Asn Lys Thr Ile Ser			
243	715 720 725			
245	aca aaa gac cag gat ttg att aaa caa tat aat aca cta ata gaa gaa	2921		
246	Thr Lys Asp Gln Asp Leu Ile Lys Gln Tyr Asn Thr Leu Ile Glu Glu			
247	730 735 740			
250	atg ctt cag gtc ctc atc tat att gtg ggt gag cgt tat gta cct gga	2969		
251	Met Leu Gln Val Leu Ile Tyr Ile Val Gly Glu Arg Tyr Val Pro Gly			
252	745 750 755			
254	gtg gga aat gtg acc aaa gaa gag gtc aca atg aga gaa atc att cac	3017		
255	Val Gly Asn Val Thr Lys Glu Glu Val Thr Met Arg Glu Ile Ile His			
256	760 765 770			
258	ttg ctt tgc att gaa ccc atg cca cac agt gcc att gcc aaa aat tta	3065		
259	Leu Leu Cys Ile Glu Pro Met Pro His Ser Ala Ile Ala Lys Asn Leu			
260	775 780 785 790			
262	cct gag aat gaa aat aat gaa act ggc tta gag aat gtc ata aac aaa	3113		
263	Pro Glu Asn Glu Asn Asn Glu Thr Gly Leu Glu Asn Val Ile Asn Lys			
264	795 800 805			
266	gtg gcc aca ttt aag aaa cca ggt gta tca ggc cat gga gtt tat gaa	3161		
267	Val Ala Thr Phe Lys Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu			
268	810 815 820			
270	cta aaa gat gaa tca ctg aaa gac ttc aat atg tac ttt tat cat tac	3209		
271	Leu Lys Asp Glu Ser Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr			
272	825 830 835			
274	tcc aaa acc cag cat agc aag gct gaa cat atg cag aag aaa agg aga	3257		
275	Ser Lys Thr Gln His Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg			
276	840 845 850			
278	aaa caa gaa aac aaa gat gaa gca ttg ccg cca cca cca cct cct gaa	3305		
279	Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro Pro Pro Pro Pro Pro Glu			
280	855 860 865 870			

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284	875 880 885	
286	atg atg tac att ctc agg acc gta ttt gag cgg gca ata gac aca gat	3401
287	Met Met Tyr Ile Leu Arg Thr Val Phe Glu Arg Ala Ile Asp Thr Asp	
288	890 895 900	
291	tct aac ttg tgg acc gaa ggg atg ctc caa atg gct ttt cat att ctg	3449
292	Ser Asn Leu Trp Thr Glu Gly Met Leu Gln Met Ala Phe His Ile Leu	
293	905 910 915	
295	gca ttg ggt tta cta gaa gag aag caa cag ctt caa aaa gct cct gaa	3497
296	Ala Leu Gly Leu Leu Glu Glu Lys Gln Gln Leu Gln Lys Ala Pro Glu	
297	920 925 930	
299	gaa gaa gta aca ttt gac ttt tat cat aag gct tca aga ttg gga agt	3545
300	Glu Glu Val Thr Phe Asp Phe Tyr His Lys Ala Ser Arg Leu Gly Ser	
301	935 940 945 950	
303	tca gcc atg aat ata caa atg ctt ttg gaa aaa ctc aaa gga att ccc	3593
304	Ser Ala Met Asn Ile Gln Met Leu Leu Glu Lys Leu Lys Gly Ile Pro	
305	955 960 965	
307	cag tta gaa ggc cag aag gac atg ata acg tgg ata ctt cag atg ttt	3641
308	Gln Leu Glu Gly Gln Lys Asp Met Ile Thr Trp Ile Leu Gln Met Phe	
309	970 975 980	
312	gac aca gtg aag cga tta aga gaa aaa tct tgt tta att gta gca acc	3689
313	Asp Thr Val Lys Arg Leu Arg Glu Lys Ser Cys Leu Ile Val Ala Thr	
314	985 990 995	
316	aca tca gga tcg gaa tct att aag aat gat gag att act cat gat	3734
317	Thr Ser Gly Ser Glu Ser Ile Lys Asn Asp Glu Ile Thr His Asp	
318	1000 1005 1010	
320	aaa gaa aaa gca gaa cga aaa aga aaa gct gaa gct gct agg cta	3779
321	Lys Glu Lys Ala Glu Arg Lys Arg Lys Ala Glu Ala Ala Arg Leu	
322	1015 1020 1025	
324	cat cgc cag aag atc atg gct cag atg tct gcc tta cag aaa aac	3824
325	His Arg Gln Lys Ile Met Ala Gln Met Ser Ala Leu Gln Lys Asn	
326	1030 1035 1040	
328	ttc att gaa act cat aaa ctc atg tat gac aat aca tca gaa atg	3869
329	Phe Ile Glu Thr His Lys Leu Met Tyr Asp Asn Thr Ser Glu Met	
330	1045 1050 1055	
332	cct ggg aaa gaa gat tcc att atg gag gaa gag agc acc cca gca	3914
333	Pro Gly Lys Glu Asp Ser Ile Met Glu Glu Glu Ser Thr Pro Ala	
334	1060 1065 1070	
336	gtc agt gac tac tct aga att gct ttg ggt cct aaa cgg ggt cca	3959
337	Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly Pro Lys Arg Gly Pro	
338	1075 1080 1085	
340	tct gtt act gaa aag gag gtg ctg acg tgc atc ctt tgc caa gaa	4004
341	Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile Leu Cys Gln Glu	
342	1090 1095 1100	
344	gaa cag gag gtg aaa ata gaa aat aat gcc atg gta tta tcg gcc	4049
345	Glu Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val Leu Ser Ala	
346	1105 1110 1115	
349	tgt gtc cag aaa tct act gcc tta acc cag cac agg gga aaa ccc	4094

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.



VERIFICATION SUMMARY

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L:2834 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18